

EXHIBIT 16

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☒ Use Mega BLAST Strand option

Open gap and extension gap penalties
gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file
or sequence in FASTA format from: to:

```
DTGNSPYESTLTHALSSQFMLSISEASUNQLKSDUUFSGNLNVPHTGWQGLWSWGWAQIQ  
DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS  
AELTPSDHPPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT  
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLAKLVGLYSYGDHNCCHFFYTQGENLTSQGT  
FRSQTMGGAFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV  
LVPIGVKGSFPMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:

```
VAGLEKDPVA
```

PT 7CT2

Murder
Enf. Immunity
61:4406, 1993

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955 *PHPO clone ATCC PTA 2462*

Sequence 2 lcl|seq_2 Length 10 *PTTCTZ*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

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Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

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```
DYGNSTYESTDLTRALSSQFLSLSEASUNQLRSDUUFSGNLNVPHYGWQGLWSWGWAQV  
DPEPASSATITDPKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS  
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT  
KLNERYAKNNVSSKNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTGGENLTSQGT  
FRSQTMGGAVFFDLPMKPPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSPSTKTPLINV  
LVPIGVKGSFMNATQRPQAWTVLAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

PTSDVAGLEKDFVA

PT 7 C + 4

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequ nces results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**

x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955 **PMPE ATCC PTA 2462**

Sequence 2 lcl|seq_2 Length 15 **PT7C4**

No significant similarity was found

BLAST 2 SEQUENCES

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Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

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```
DYGNSTYESTDLTHALSSQPLLSISEASDNLKRSDDMDFSGLNVFHYGWQLWSWGWAQV  
DPEPASSATITDPKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS  
AELTPSDHPPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT  
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLAKLVGLYSYGDHNCCHFTQGENLTSQGT  
FRSQTMGGAVFFDLPMKFFGSTHILTAPFLGALGIYSSLSHFTVEGAYPRSFSTKTPLINV  
LVPIGVKGSFMNATQRPQAWTVELAYQFVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

PTTSDVAGLEKDPKD

PT 7c+5

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**

x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955 **PMPE ATCC PTA 2462**

Sequence 2 lcl|seq_2 Length 15 **PT7CTS**

No significant similarity was found

BLAST 2 SEQUENCES

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Open gap and extension gap penalties

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Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DTGNSFTESTDTHALSSQPLSLSEASDNLQRSDDMDFSGLNVPHIGWGLWSWGWAKTV
DPEPASSATITDPKKNRFRHTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGVFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLAKLVGLYSYGDHNCCHFYTGQENLTSQGT
FRSQTMGGAFFDLPMKPPGSTHILTAFFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVLAYQPVLRYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHPQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

NPASTTSDVAGLEKDPVA

CT7CT7

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955

Sequence 2 lcl|seq_2 Length 18

No significant similarity was found

PMPE clone PTA 2462
~~PTA 2462~~ PTA 2462

BLAST 2 SEQUENCES

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Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DYGNSTFYESTDLTRALSSQFMLSISEASUNQLRSDDMFSGNLNVPHYGWQLLWSGWAKTQ
DPEPASSATITDPKKANRFHRTLLLTWLPAGYVFPSPKHSPLIANTLWGNMLLATESLKNS
AELTPSDHPPWGI TGGGLGMMVYQEPRENHPGFHMRSSGYFAGMLAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTQGENLTSQGT
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTVEGAYPRSPSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVELAYQPVLRYQLEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
NPASTTSDVAGLEKDEPKD
```

P-T7C+8

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **10.0** wordsize: **3** Filter: ☒ **Align**Sequence 1 lcl|seq_1 Length 955 **PMPE ATCC PTA 2462**Sequence 2 lcl|seq_2 Length 18 **PTTCT**

No significant similarity was found